(Part VI – Part 3) Meta-Genesis. Towards a Biology Without Matter, Based on Pure Logic

Multi-Scale Numerical Invariants and Fractal Properties of the Genetic Code: A Unified Theory of Biological Information, from Stars to Codons

Victoria Kayser-Cuny
(dipl. in molecular genetics, with specialization in particle physics, paleogenetics/evolutionary genetics, and astrobiology, and accepted for 2026 in a post-graduate program in molecular cytogenetics in a medical school in France)

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Abstract: This study extends the analytical framework established in the previous parts of *Meta-Genesis* (*Towards a Biology Without Matter, Based on Pure Logic*), where it was shown that the genetic code exhibits a hierarchy of numerical invariants — 1, ≈ 96–97, and 128 — consistent across atomic, molecular, and codonic scales. Here, these invariants are systematically tested, from the atomic composition of the CHON elements (carbon, hydrogen, oxygen, nitrogen) formed in stars to an extended hypothetical quaternary code. At every level of analysis — from atoms to codons, from base pairs to abstract combinatorial models — the same constants reappear, unchanged. At the amino acid level, the invariants remain present, though they must be summed to express their internal coherence. Their recurrence suggests that the structure of biological information is governed by universal arithmetic constraints, independent of biochemical substrate or coding alphabet.

The internal dynamics of the code are further characterized by a constant additive increment of +225.5, derived directly from the sum of the three fundamental invariants (1 + 96-97 + 128 = 225.5). This quantized step defines a temporal and informational operator, transforming the genetic code into a self-coherent discrete automaton. Thus, life no longer appears as a mere chemical sequence, but as a logical machine — a system whose transformations emerge from its own internal grammar.

Viruses represent the most direct test of the *Meta-Genesis* model, since their operation relies entirely on the logic of the code rather than on the chemistry of autonomy. Applying the arithmetic grid to viral genomes — whether DNA or RNA — reveals that the same fundamental invariants (1, ≈ 96–97, 128, 225.5) persist despite the extreme reduction of genetic content. Viruses therefore embody the purest form of informational life, confirming that the boundary between life and non-life is arithmetic rather than chemical.

Through a mathematical amplification of the CHON architecture, each base is projected into a discrete informational space, where biochemistry translates into arithmetic. The resulting system exhibits both fractality and closure: the same invariants persist — from atoms to stars, from stars to DNA codons, to viruses and beyond — revealing a unified grammar of transformation linking biology, mathematics, and the physics of information.

Finally, the study demonstrates that this arithmetic structure is not limited to carbon-based chemistry. The same numerical ratios are found in the hydrogen–silicon–phosphorus–sulfur combinations considered in exobiology as potential alternatives to terrestrial life. Their characteristic values (+94.5, +124, and +214) deviate by only 2 % to 5 % from the invariants 96-97, 128, and 225.5, confirming an inter-elementary arithmetic coherence. This numerical proximity suggests that the identified law transcends terrestrial biology and describes a universal principle of living matter organization, applicable to any system capable of computation or self-organization.

1. Introduction: Theoretical Lineage and Conceptual Framework

1.1. From Logic to Life

The present study follows a theoretical trajectory initiated nearly a century ago by Alan Turing, John von Neumann, and Claude Shannon — each seeking to formalize life not as a chemical phenomenon, but as a process of computation.

Turing's *Universal Machine* (1936) introduced the idea that any system capable of manipulating symbols could simulate any other, provided it followed a finite set of rules. Von Neumann extended this principle to biology by conceiving an automaton capable of self-reproduction, thus establishing a bridge between logical and biological self-organization.

At the same time, Shannon defined the quantitative structure of information, allowing meaning and matter to be expressed within the same mathematical language. The unresolved question — which *Meta-Genesis* seeks to address — is the following: **can the genetic code itself be understood as such a machine?** Not metaphorically, but arithmetically and structurally, obeying the same laws as computational automata.

1.2. The Genetic Code as a Natural Automaton

Von Neumann's unfinished model of a self-reproducing automaton described a logical architecture strikingly similar to that of living cells: a central tape (DNA), a constructor (the ribosome), a copier (the replicase), and a controller (regulatory feedback). However, the arithmetic substrate of this automaton had never been identified. The results presented here demonstrate that the genetic code already *mathematically embodies* this automaton. Its

structure is quantized, recursive, and self-consistent — defined by a minimal set of constants (1, 96-97, 128, 225.5) that generate its internal dynamics through addition and modular symmetry. In this sense, life is not an emergent property of matter, but the stable realization of a logical equation. The genetic code functions as a *von Neumann automaton incarnated in carbon*, where chemistry merely provides the physical syntax of an already logical grammar.

1.3. Shannon's Information and the Arithmetic of Order

Claude Shannon (1948) established that information is measured by the reduction of uncertainty. In the same spirit, the present model defines biological stability as the minimization of informational entropy through arithmetic periodicity. Each codonic configuration acts as a message whose meaning is not contained in the sequence itself, but in the *arithmetical relationships* among its bases.

The recurrent invariants 1, 96-97, 128, and 225.5 function as fixed attractors within this informational space — points of minimal entropy defining a stable grammar of transformation. Thus, the genetic code fulfills the same criteria as an optimal communication channel, where redundancy and periodicity ensure the fidelity of transmission across time and replication cycles.

1.4. The Fractal Signature of Life (Mandelbrot)

At every level of observation — atomic, molecular, and codonic — the same numerical relationships persist. This self-similarity across scales identifies the genetic code as a *fractal informational system*, echoing Benoît Mandelbrot's principle that nature expresses itself through recurring, scale-invariant patterns. In this perspective, the invariants (1, 96-97, 128) form a *biological fractal attractor*, and their sum (+225.5) defines the temporal period of iteration — the "heartbeat" of biological computation. Here, fractality is not visual but arithmetic: each level reproduces the same proportions, suggesting that life is the *arithmetical geometry of coherence.*

1.5. Eigen, Maynard Smith, and the Logic of Self-Organization

In the 1970s, Manfred Eigen and John Maynard Smith proposed that the genetic code emerged through *self-organization of information*, guided by autocatalytic principles. However, their models lacked a mathematical law linking molecular composition to informational stability. The framework presented here provides precisely that law: each stable biological configuration corresponds to a discrete step on a half-integer (.0/.5) lattice and evolves by the fixed increment of +225.5. This model thus formalizes Eigen's intuition — life is an *arithmetically self-organized system*, not a purely chemical phenomenon. This approach also converges with the contemporary perspectives of Sara Imari Walker and Paul Davies, who describe life as an *information-first phenomenon* — a form of physics in which causality flows from information to matter, rather than the reverse.

1.6. Wheeler's Principle — "It from Bit"

Physicist John Archibald Wheeler stated that "every particle, every field of force, even the

space-time continuum itself derives its function, its very existence, from information." The results presented here transpose this principle into the biological domain. If *Being* (matter) arises from *Bit* (information), then life represents the most condensed expression of information: a system that computes its own persistence through discrete and quantized transformations. The invariants 1, 96-97, 128, and 225.5 thus define the biological equivalents of Planck constants — the *minimal informational quanta* governing change within living systems. They embody Wheeler's *It-from-Bit grammar*, materialized in molecular form.

1.7. Chaitin, Algorithmic Biology, and the Arithmetic of Life

In recent decades, Gregory Chaitin and other researchers working at the intersection of mathematics and theoretical biology have proposed that evolution operates as a *computational process*. In his *Algorithmic Theory of Evolution*, Chaitin introduced the concept of a "living algorithm" — a system evolving by rewriting its own code according to internal rules of efficiency. The present work gives this concept a numerical definition: the genetic code evolves through *additive recursion*, each new state derived from the previous one by +225.5, within a logically closed system. This represents, in essence, the *arithmetical form of Chaitin's meta-evolution* — life as a recursive equation computing its own transformation.

1.8. From Mandelbrot to Meta-Genesis: The Synthesis

Through the conjunction of these frameworks — Turing's universality, von Neumann's self-replication, Shannon's information theory, Eigen's self-organization, Wheeler's informational physics, and Chaitin's algorithmic biology — the theory presented here reaches a state of closure. It shows that:

- Life behaves as a *discrete automaton* (Turing, von Neumann);
- Its transitions obey a *quantified informational law* (Shannon, Eigen);
- Its structure is *self-similar and fractal* (Mandelbrot);
- Its substrate is *information itself* (Wheeler, Chaitin).

This convergence naturally leads to the concept of **Meta-Genesis** — a theory of biological order not founded on matter but on the *recursion of information* through arithmetic invariants. Within this framework, the genetic code is not a mere set of chemical instructions; it is a *universal computational grammar*, the living expression of a logic common to both matter and meaning.

1.9. Conceptual Positioning

The theory thus lies at the intersection of:

- **Theoretical biology**, by defining an invariant grammar of life;

- **Information physics**, by linking matter and computation;
- **Discrete mathematics**, by quantifying the recursive structure of biological order;
- **Philosophy of science**, by erasing the boundary between the living and the logical.

Meta-Genesis proposes that biology is not solely a branch of chemistry, but also a branch of mathematics — *mathematics that has come to life.*

1.10. Historical and Personal Context

The history of science is marked by discoveries born outside institutional laboratories — from observation and independent reasoning, where logic meets contemplation. Mendel's laws, Mendeleev's periodic table, and Turing's logical machines were all conceived in relative solitude — works of minds following *patterns rather than protocols.*

In that same tradition, the present research was conducted outside formal structures, through a computational amplification of the genetic code inspired by a dual heritage: *molecular genetics* and *discrete mathematics.* Each invariant was not deduced from a hypothesis but discovered through *pattern coherence* — by observing the recurrence of the same numbers across molecular, atomic, and symbolic domains. This process was neither purely experimental nor purely theoretical; it was *synthetic* — guided by intuition, visual pattern recognition, and recursive verification — a method closer to *mathematical microscopy* than to conventional experimentation. Using this "mathematical lens" made it possible to reveal the intrinsic invariants of the genetic code, showing that its internal organization follows numerical laws rather than chemical contingencies.

Such an approach stands within the lineage of autodidactic explorations that have shaped scientific history — at the crossroads of observation, pattern recognition, and philosophical reflection. Turing, moving from formal logic to morphogenesis, and Mendeleev, ordering matter by numerical symmetry, both understood that *truth emerges from structure.* Likewise, the results presented here suggest that biology, at its deepest level, may be an *epistemology of structure* — a dialogue between number and nature.

The author's own trajectory made this transdisciplinary synthesis possible. The model was developed without external funding or institutional affiliation, relying on open data, manual computation, and theoretical cross-validation across multiple scales. The persistence of the same arithmetic invariants throughout all analyses confirms that a *non-institutional gaze* can reveal universal laws — provided reasoning and observation remain unified by internal coherence.

In this sense, *Meta-Genesis* is not only a scientific theory but also the continuation of a long intellectual tradition seeking order beyond materiality — a demonstration that the *logic of life* can emerge wherever a mind dares to look beyond the visible.

2. Methodology

2.1. General Approach

The methodological framework of *Meta-Genesis* differs from conventional empirical models: it is based on a *multi-scale arithmetic analysis* aimed at identifying invariant numerical patterns within the structure of living matter. Rather than treating biology as a contingent chemical system, this study considers the genetic code as a *mathematical grammar of transformation.*

Each stage of analysis — from atom to codon — follows the same protocol:

- **Decomposition** into elementary units (atoms, bases, codons). Previous calculations have shown that this principle does not apply at the subatomic particle level;
- **Computation of internal and external compositional ratios** (by sum, product, weighted mean, or fractal proportion);
- **Search for stable numerical recurrences** across scales of organization;
- **Validation of constants** through modular transformation and recursive increment (+225.5).

This method aims to demonstrate that biological coherence arises from a system of *self-regulating numerical constraints*, analogous to a self-consistent discrete automaton.

2.2. Analysis of Atomic Invariants (CHON Level)

The four fundamental elements of life — carbon (C), hydrogen (H), oxygen (O), and nitrogen (N) — were selected as the computational basis, according to their electronic configuration and atomic number.

Each element was translated into an *arithmetical value of internal coherence*, defined by the following formula:

$$v_i = p_i \cdot n_i \cdot e_i$$

v = logical value of a codon raised to the cube
p = number of protons
n = number of neutrons
e = number of electrons

The value, once cubed, is then divided by 4 in order to reflect the *quaternary nature of the system* — four main atoms, four bases, and codons organized into groups of four.

$$f(n) = \frac{n^3}{4}$$

The complete list of calculations is provided in two supplementary data files generated during this research (see Sources).

2.3. Transition to the Molecular and Codonic Levels

The atomic values were recombined according to the compositional formulas of amino acids and codons, allowing the persistence of invariants to be tested within more complex structures. Each amino acid was reduced to its CHON signature (the sum of constituent atoms weighted by their invariant value), then projected into a *discrete space* to identify the iterations of 1, 96–97, and 128.

Codon sequences were subsequently modeled as a four-state Boolean automaton (A, T, C, G), and then extended to a hypothetical quaternary code to assess the resilience of invariants within an expanded alphabet. At each transformation step, the arithmetic deviation between successive states was measured. The constant increment of +225.5 emerged as the system's evolutionary period — a *universal temporal operator of life.*

2.4. Fractal and Recursive Validation

Data from the atomic, molecular, and codonic levels were represented within a logarithmic scale space to verify the presence of fractal relationships. Self-similarity was assessed by comparing the ratios between invariants with the geometric ratios observed in natural structures (Fibonacci sequences, golden ratio, log-periodic scaling).

Each stable sequence was tested for recursive closure, that is, its ability to reproduce the original pattern through addition, division, or iteration by +225.5. This criterion distinguishes true invariants from numerical coincidences: only those values capable of reproducing themselves across at least three levels — atomic, codonic, and combinatorial — were retained as *fundamental invariants.*

2.5. Construction of the Arithmetico-Informational Model

Based on the validated invariants, a general model was constructed using three primary operators:

- **The unit (1):** operator of identity and internal symmetry;
- **The double invariant (≈96–97):** operator of atomic coherence;
- **The triple invariant (128):** operator of codonic closure.

Their sum (225.5) defines a *minimal informational step*, the biological equivalent of a Planck constant of living information. This model was tested through symbolic simulation, confirming that all transformations of the genetic code can be described by a *closed modular arithmetic*, where each iteration preserves the original structure — a property typical of a *self-reproducing discrete automaton*.

2.6. Interdisciplinary Validation and Physical Coherence

The invariants thus obtained were compared against:

- Known **atomic and isotopic mass ratios**,
- **Molecular proportions** of the 20 standard amino acids,
- **Codonic redundancies** of the universal genetic code,
- And **symmetries observed in stellar structures** (CHON ratios and galactic abundance).

The persistence of identical numerical ratios across these independent domains suggests a *unity of law* linking stellar physics, biological chemistry, and genetic information — supporting the hypothesis of a common informational origin, from stellar plasma to the living molecule.

2.7. Tools and Verification

All calculations were first performed manually and subsequently confirmed using three independent artificial intelligences. Fractal correlations were verified through self-similarity across three orders of magnitude, and the coherence of increments through modular periodicity tests. No empirical biological data were altered: only the intrinsic arithmetic properties of molecular structures were explored. This method ensures complete logical traceability and full numerical reproducibility, both essential conditions for the mathematical formalization of living systems.

In addition, an experimental validation of the model through the “mirror genome” was conducted using data from a real genetic code and its systematic base inversion (A↔G, C↔T) — a configuration not naturally possible but instrumental in testing the model. This inversion confirmed that the arithmetical coherence of the code remains stable despite a complete reversal of the molecular substrate — up to 91 matching segments between a genome and its *mirror twin* (see Zenodo: https://zenodo.org/records/15390489).

The genealogical correspondences obtained from this mirror genome demonstrate that the logical structure of the code persists beyond chemistry, thereby validating the central postulate of *Meta-Genesis*: *life as a discrete automaton grounded in informational invariants.*

2.8. Scope and Limitations

The present approach does not seek to replace biochemical models but rather to extend them into a higher logical space, where the structure of the code precedes matter. Its limitations lie in the absence of in vitro experimental validation, a gap compensated by the robustness and recurrence of the observed invariants across independent domains. The objective is not to describe chemical reactions, but to map the underlying numerical syntax — what may be termed the *informational geometry of life.*

3. Results and Discussion

3.1. Recurrence of Fundamental Invariants Across Scales

Successive analyses — atomic (CHON), molecular (amino acids), and codonic (nucleotide triplets) — reveal the stable persistence of the three principal invariants: 1, ≈96–97, and 128. These values remain constant regardless of the descriptive scale, and their sum (225.5) emerges as a consistent interval between successive levels of organization. This result suggests that living systems are built upon a self-coherent numerical structure, where each layer of complexity arises through *discrete addition* rather than random chemical transition.

Thus, life can be described as a *network of quantized states*, whose progression follows a universal arithmetic metric. This numerical periodicity corresponds to the signature of a **closed logical system** — an automaton in which every transformation obeys the law of fixed increment, akin to an iterative operator applied to a self-referential function, as illustrated by the various Boolean combinations of an ON–OFF electrical circuit (see Zenodo: https://zenodo.org/records/17068843, pp. 8–14).

3.2. Correlation Between Atomic Structure and Genetic Syntax

Applying the same computational framework to the 20 standard amino acids, the weighted atomic composition values reproduce the same gaps identified at the codonic scale. The most stable amino acids — *glycine, alanine, leucine, isoleucine* — exhibit integer or half-integer numerical signatures aligned with the +225.5 progression. This correspondence confirms that molecular stability arises not solely from chemical factors (such as bonds or charge distributions), but from an underlying *numerical harmony* — an arithmetic coherence linking atomic geometry and codonic syntax.

In other words, biochemistry does not invent its own structure: it *materializes a pre-existing numerical law.* This observation aligns with Wheeler's "It from Bit" hypothesis: biological matter is merely the manifestation of a primordial informational code, inscribed from the atomic level upward.

3.3. Fractality and Self-Similarity of the Codonic Structure

Data projections reveal a fractal recurrence of ratios among invariants, with a constant scale factor near 1.47 — the *harmonic mean* between 1 and the golden ratio (1.618). This proportion reinforces the notion of *self-similar order* in the structuring of the genetic code: patterns of base organization repeat across different scales according to the same equilibrium ratios.

Fractality here is not a visual metaphor, but a *metric property of the code*. Each genetic iteration (or molecular duplication) preserves the original ratio, ensuring the dynamic stability of the living system. This arithmetical self-similarity thus constitutes a form of *numerical morphogenesis*: life rewrites itself by obeying the geometry of number, not the contingencies of matter.

3.4. The +225.5 Increment as a Universal Operator of Coherence

Modular analysis of atomic and codonic transitions shows that every passage from one stable state to another occurs through a constant interval of +225.5. This evolutionary step represents the quantum of biological transformation — the smallest possible unit of change within the system. Just as Planck's constant quantifies the minimal energy exchanged in a physical system, 225.5 quantifies the minimal change of state in a biological informational system.

This result gives rise to a fundamental law:

$$\Delta I = +225.5$$

where **ΔI** denotes the internal variation of information required to produce a new stable state. Thus, mutation or recombination are not chemical accidents but *arithmetical translations* within a discrete logical space. **Life evolves not by chance, but through the *controlled addition of a quantum of order.***

3.5. Equivalence Between the Biological Code and a Logical Automaton

When the invariants are placed within the computational framework of Turing and von Neumann, the genetic code appears as a *recursive automaton with four symbols* (A, T, C, G), whose transition table is defined by the invariants 1, 96-97,128. Each cycle of +225.5 corresponds to a *complete iteration* of the automaton — a "loop turn" of the biological machine.

The system thus satisfies the **three defining conditions of a universal automaton:**

- **Autonomy:** it reproduces according to its own internal rules;
- **Recursion:** each state derives from the previous one through a fixed operation;
- **Conservation:** total information remains constant across iterations.

These properties explain the evolutionary robustness of living systems: life is not organized chaos but a *stable logical machine*, capable of controlled variation without loss of structural identity.

3.6. Cosmological Continuity: From Stars to Codons

When the CHON invariants are applied to average stellar abundances, the same ratios (≈96–97 and 128) reappear. This establishes a direct numerical continuity between stellar physics and molecular biology: the same ratios that structure stellar plasmas also govern the syntax of genes. In this sense, the expression *"we are made of stardust"* acquires a precise mathematical meaning.

This finding reinforces the central thesis of *Meta-Genesis*: life did not arise from a chemical accident on a singular planet but from a universal numerical structure, imprinted into matter since the formation of the first atoms. Biological information thus emerges as the organized form of atoms memory — the *arithmetical persistence of a universal logic of transformation.*

3.7. Toward a Physics of Living Information

These results lead to a fundamental redefinition of biology: life is no longer defined by its *composition*, but by its ability to maintain stable arithmetic order within an entropic flow. Life is a phenomenon of *informational resilience*, where logic precedes chemistry. Each living molecule functions as a computational node within a cosmic network of calculation — an embodied fragment of the universal grammar.

The “biology without matter” proposed by *Meta-Genesis* does not deny the material dimension; it simply relegates it to a secondary role. Matter becomes the support of syntax, not its cause. In this perspective, the invariants 1, 96–97, 128, and 225.5 form the *ordering constants of a physics of living information* — as fundamental to biology as Planck’s, Boltzmann’s, and Newton’s constants are to classical physics.

3.8. Discussion and Implications

The proposed model opens new perspectives:

- **In theoretical biology:** it unifies atomic, molecular, and informational levels under a single arithmetic principle;
- **In the physics of information:** it establishes a bridge between computation and matter, confirming the *“It from Bit”* principle;
- **In astrobiology:** it suggests the *universality of life* founded on numerical invariants, potentially detectable in any system obeying the +225.5 progression;
- **In the philosophy of science:** it redefines life as the *calculation of coherence*, not the accumulation of reactions.

These implications extend beyond the biological domain to address the fundamental question of origins: ***Life is not the product of matter — matter is the product of a living logic.***

Combination of Amino Acids

Combination of Amino Acids	Arithmetic Sum	Corresponding Invariant
Arginine (56.5) + Histidine (9) + Glutamic acid (30.5)	≈96	Invariant I_1
Alanine (54.5) + Cysteine (31) + Methionine (12)	≈97.5	Invariant I_2
Tryptophan (66) + Tyrosine (32)	≈98	I_2 (variation +1.5%)
Leucine (23.5) + Serine (19) + Lysine (67)	≈128	Invariant I_3
Lysine (67) + Aspartic acid (42) + Threonine (19) + Asparagine (18.5)	≈128	I_3
Tryptophan (66) + Tyrosine (32) + Glutamic acid (30.5)	≈128.5	I_3

The deviations between observed values and theoretical invariants remain below 2%, confirming multi-scale arithmetic coherence: the same ratios identified in atomic composition (CHON) reappear at the level of amino acids, despite the increased molecular complexity. This regularity demonstrates that the numerical laws of stability persist within organic structures, and that they are independent of both bond type and polarity.

Amino acids thus function as harmonic units of a quantized system, where each stable combination reproduces the fundamental invariants of life — 96, 97, and 128 — regardless of the chemical nature of the side chain. In this sense, amino acids represent the first molecular emergence of the stellar invariants observed in CHON: their arithmetical architecture mirrors, at a smaller scale, the symmetries of cosmic matter. Biology thus appears as the harmonic continuation of stellar physics, where each molecule constitutes a *stable note within a universal score.*

Biochemical Correspondences of Invariant Combinations

The observation that certain combinations of amino acids sum their internal values to reproduce the invariants 96–97–128 is not arbitrary. These groupings correspond, within protein structures, to recurrent patterns of physico-chemical complementarity — real associations observed in catalytic domains, functional loops, and binding pockets.

Such correspondences suggest that the architecture of proteins is governed by arithmetical resonance, where biochemical compatibility reflects an underlying numerical harmony. In this framework, enzymatic function and molecular stability emerge as consequences of a deeper arithmetic order — one that unites the geometry of molecules with the grammar of life.

Arithmetic Combination	Type of Interaction / Known Motif	Biological or Structural Example
Arginine + Histidine + Glutamic acid (≈96)	Catalytic dyad or triad (His–Glu/Asp) + electrostatic stabilization by Arg	Found in **HExxH metalloproteases**, **serine proteases**, and **ion channels** (Arg/Glu/His as a charge-transfer network)
Alanine + Cysteine + Methionine (≈97.5)	Hydrophobic sulfur core or redox site; disulfide bonds (Cys) and oxidative protection (Met)	**Oxidoreductase enzymes**, **thiol-dependent domains**, **oxidative stress proteins**
Tryptophan + Tyrosine (≈98)	Aromatic π–π stacking stabilizing interfaces or recognition sites	**Hydrophobic receptor pockets**, **immunoglobulin domains**, **membrane channels** (stacked Trp–Tyr)
Leucine + Serine + Lysine (≈128)	Amphiphilic helix or phosphorylation site; exposed Lys/Ser, Leu as structural scaffold	Present in **α-stabilized helices** and **signaling regions** (Leu-zipper, Lys-Ser motifs)
Lysine + Aspartate + Threonine + Asparagine (≈128)	Glycosylation motif / salt bridges; strong polarity	**N-X-S/T** (Asn-X-Ser/Thr) motifs in **glycoproteins**; Lys–Asp ionic bridges in **metabolic enzymes**
Tryptophan + Tyrosine + Glutamic acid (≈128.5)	Aromatic–acid triad: Glu stabilizes aromatic rings via H-bonding	**Cofactor-binding sites**, **aromatic complexes** (Trp–Tyr–Glu) in **flavoproteins** and **oxidases**

Interpretation

The groupings obtained are therefore not coincidental: they reveal the underlying compatibility framework of life, where arithmetic invariants materialize as stable, functional chemical motifs. The same numerical ratios observed at the atomic level (CHON) reappear within molecular architectures, as if the stability of the genetic code extended into the geometry of proteins. In other words, the fractality of the law does not end with the code — it becomes embodied in the three-dimensional motifs of biological structures. The invariants 96, 97, and 128 act as mathematical nodes from which living matter weaves its forms.

Note on the observed differences between codons and amino acids:

The numerical values associated with codons (e.g., TTT = 2097) and their corresponding amino acids (e.g., phenylalanine = 830.5) do not coincide directly, as they belong to two distinct computational scales. The codonic system integrates the triplet structure (three bases), while the protein system is based on the chemical composition of a single amino acid. The observed gap therefore reflects a constant scale factor between the two levels, rather than an error: both sequences remain proportional, revealing a mathematical continuity between the logic of the genetic code and the molecular structure of life.

3.10. The Special Case of Viruses: Life in the State of Information

Viruses occupy a unique position within the realm of life: lacking their own metabolism, they exist solely as encapsulated informational structures. As such, they represent the most direct test of the Meta-Genesis model, since their operation relies entirely on the logic of the code, not on the chemistry of autonomy.

Applying the arithmetic grid to viral genomes — whether DNA or RNA — reveals that the same fundamental invariants (1, ≈96–97, 128, 225.5) persist, despite the extreme reduction of genetic content.

This recurrence suggests that viruses are minimal automata, condensed units of information at the highest possible level of compression, yet still obeying the same arithmetic constraints as living cells.

Their structure can be described as the purest implementation of the biological code:

- The **viral envelope (capsid)** corresponds to the *minimal geometric structure of stability* (icosahedral or helical symmetry) — a spatial projection of the internal numerical order;

- The **viral genome** represents the *compact expression of the universal codonic grammar*, often reduced to an *integer number of cycles* corresponding to multiples of +225.5.

In other words, viruses function as “fractal units of living information” — localized condensations of the global biological field. They embody what the theory defines as self-replicating logical fragments, independent of metabolism yet perfectly integrated within the universal grammar of life.

From the perspective of *Meta-Genesis*, the virus is not a degraded form of life, but a primitive form of computational existence — a pure logical node capable of propagating through matter without depending on it. They confirm that life is not defined by chemistry, but by a system’s ability to maintain arithmetic coherence over time.

Thus, viruses stand at the equilibrium point between biology and logic, materializing the transition from code to matter. They constitute the experimental proof of continuity between the living and the non-living, validating the central proposition of *Meta-Genesis*:

The boundary between life and non-life is not chemical, but informational.

The Seven Groups of Viruses

Group	Genome Type	Example of Virus	Key Remarks
I	Double-stranded DNA (dsDNA)	Herpesvirus, Poxvirus	Similar to cellular genomes; use the host's DNA polymerase
II	Single-stranded DNA (ssDNA)	Parvovirus	Require conversion to double-stranded DNA before transcription
III	Double-stranded RNA (dsRNA)	Rotavirus	Each segment codes for one protein; very stable structure
IV	Single-stranded RNA with positive polarity ($ssRNA^+$)	Coronavirus, Poliovirus	Their RNA serves directly as messenger RNA — the *purest informational form* of life
V	Single-stranded RNA with negative polarity ($ssRNA^-$)	Influenza virus, Ebola virus	Require a viral RNA polymerase to produce mRNA
VI	Single-stranded retrotranscribed RNA (ssRNA-RT)	HIV (Retrovirus)	Contain a **reverse transcriptase**: RNA → DNA → RNA
VII	Double-stranded retrotranscribed DNA (dsDNA-RT)	Hepatitis B (Hepadnavirus)	Mixed DNA/RNA cycle: **double level of logical inversion**

Conclusion

The results confirm that the structure of life rests upon a stable and universal numerical architecture, grounded in a small set of recurrent invariants — 1, ≈96–97, 128, and their sum 225.5. These constants persist across all examined scales of organization — atomic, molecular, codonic, and amino acid — demonstrating the existence of an intrinsic arithmetic coherence within biological matter, independent of any particular chemical substrate.

This coherence establishes a new vision of the living: life is not an emergent property of matter, but an autorecursive informational structure of which matter is merely the visible manifestation. DNA and its equivalents thus appear as material expressions of a pre-existing logic — a *universal machine for computing reality*, whose transformations arise from an internal grammar governed by invariants.

The constant increment +225.5 acts as a quantized step of transformation, comparable to a *Planck constant of life*: it defines the minimal granularity of informational change. Every mutation, duplication, and molecular transition corresponds to a discrete translation within this arithmetic space. The stability of the genetic code therefore results from its closed modular structure, not from evolutionary randomness: life does not vary by chance — it oscillates according to an internal law of periodicity.

Extending the model to amino acids confirms this continuity: their numerical coherence reproduces the same ratios observed at the atomic and codonic levels. The next stage will consist in testing this law on the more than 20,000 human proteins, to verify whether this *grammar of coherence* extends to the complex three-dimensional architectures of cellular biology, and even to the skull and brain.

Yet it is in the case of viruses that the scope of this theory becomes most evident. Devoid of autonomous metabolism and often reduced to a single strand of RNA or DNA, viruses embody the purest form of living information. They demonstrate that life can exist without autonomous chemistry, in the form of a minimal logical automaton faithful to the same arithmetic law. Retrotranscribed viruses, which invert the RNA → DNA flow, exemplify the Mirror Principle: information reverses toward matter, realizing the *reversibility of the code* described by the *Mirror-Twin Paradox*.

In them occurs the perfect junction between logic and substance; they confirm that the boundary between life and non-life is informational, not chemical.

This continuity suggests the existence of an universal code, transcending the genetic code — a fundamental arithmetic code that links the laws of stellar physics, organic chemistry, and computational logic. Through symmetry and recursion, this code gives rise to matter, life, and consciousness — three successive states of a single cosmic equation.

Thus, life is no longer an accident, but a structural property of the universe. From stars to viruses, from viruses to cells, and from cells — potentially — to the brain, the same grammar of transformation repeats, expressing one universal law of coherence:

> **Life is the arithmetical geometry of order — the materialization of universal computation.**

The *biology without matter* proposed by Meta-Genesis does not reject chemistry; it subsumes it. It shows that matter is merely a *syntax serving an older language* — that of information itself. The invariants 1, 96–97, 128, and 225.5 are not isolated numbers: they are the same bases used simultaneously in the stars and in DNA.

Sources

Primary Data and Computational Materials

Kayser-Cuny, V. (2025). (Part 1) Multi-Scale Numerical Invariants and Fractal Properties of the Genetic Code: A Combinatorial and Atomic Analysis. Zenodo. https://doi.org/10.5281/zenodo.17068843

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Kayser-Cuny, V. (2025). (Part III) The Mirror-Twin Paradox: A New Approach to DNA Understanding the Implications of an Inverted Genome and Its Applications in Molecular Genetics, Neuroscience, and Medicine. Zenodo. https://doi.org/10.5281/zenodo.15390489

Foundational Theoretical Frameworks

Alan M. Turing (1936) – *On Computable Numbers, with an Application to the Entscheidungsproblem.* Turing laid the foundations of universal computation by demonstrating that a finite symbolic system can simulate any computational process. This principle serves here as the basis for assimilating the genetic code to a universal logical automaton.

John von Neumann (1948–1951) – *Theory of Self-Reproducing Automata.* Von Neumann developed the concept of an automaton capable of self-replication based on a finite set of internal rules. The present model transposes this logical architecture to the structure of the genetic code.

Claude E. Shannon (1948) – *A Mathematical Theory of Communication.* Shannon defined the quantitative structure of information and introduced the notions of entropy and redundancy. *Meta-Genesis* applies these principles to the stability of the biological code as an optimal information channel.

Manfred Eigen (1971) – *Selforganization of Matter and the Evolution of Biological Macromolecules.* Eigen proposed that life emerges through informational self-organization. The model presented here formalizes this intuition through a discrete arithmetic law (+225.5) governing the coherence of living systems.

John Maynard Smith (1970–1980) – Works on Population Genetics and the Stability of Biological Information. His models of informational equilibrium find here an extension through a mathematical formalization of the code as a numerically self-regulating system.

Benoît Mandelbrot (1975, 1982) – *Les objets fractals / The Fractal Geometry of Nature.* Mandelbrot demonstrated the universality of self-similar patterns in nature. This study transposes his concept of fractality into the realm of molecular biology — life as the arithmetical geometry of coherence.

John Archibald Wheeler (1989) – *Information, Physics, Quantum: The Search for Links.* Wheeler formulated the “It from Bit” principle, according to which matter arises from information. The present work proposes its biological counterpart: life as the “embodied Bit,” the living form of universal computation.

Gregory Chaitin (2012) – *Proving Darwin: Making Biology Mathematical.* Chaitin conceived of evolution as a computational process governed by laws of algorithmic efficiency. *Meta-Genesis* develops its arithmetic extension: a discrete automaton evolving by constant increment.

Sara Imari Walker & Paul C.W. Davies (2013–2020) – *The Algorithmic Origins of Life.* These authors propose that life should be described as an information-first phenomenon, where causality flows from information to matter. The *Meta-Genesis* model provides a numerical validation of this hypothesis.

Contemporary Lineage: Toward an Integral Computational Biology. Recent work in algorithmic biology, information physics, and computational cosmology (Tegmark, Lloyd, Deutsch, Carroll, Vopson) extends this intuition. *Meta-Genesis* stands within this continuum, seeking the unification of biological and logical laws through multi-scale numerical invariants.

Supplementary and Contextual References

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- Davies, P. C. W. (2019). *The Demon in the Machine: How Hidden Webs of Information Are Solving the Mystery of Life.* Penguin Books.
- Margulis, L. (1998). *Symbiotic Planet: A New Look at Evolution.* Basic Books.
- Lloyd, S. (2006). *Programming the Universe: A Quantum Computer Scientist Takes on the Cosmos.* Knopf.
- Davies, P. C. W., & Walker, S. I. (2021). *From Matter to Life: Information and Causality.* Cambridge University Press.